The phenomenon of monodromy in 2D persistent homology

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Outline

Let us recall some concepts in persistent homology

The importance of lines with slope 1 in 2D persistent homology

The need for coherent matchings

The phenomenon of monodromy

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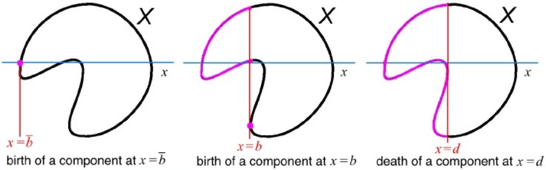
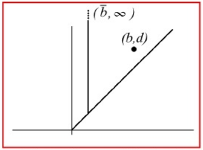
Let us recall what a persistence diagram is

The persistence diagram $\mathrm{Dgm}(\varphi)$ is a collection of points of $\mathbb{R}^2$ associated with a continuous filtering function $\varphi : X \to \mathbb{R}$. Each point $(b, d) \in \mathrm{Dgm}(\varphi)$ describes the time of birth b and the time of death d of a homological class. For technical reasons, every point (x, x) is added to the persistence diagram.



birth of a component at $x = \overline{b}$ birth of a component at $x = b$ death of a component at $x = d$



Persistence diagram of the function x

The presence of a point (b,d)

in the persistence diagram of $\varphi : X \to \mathbb{R}$

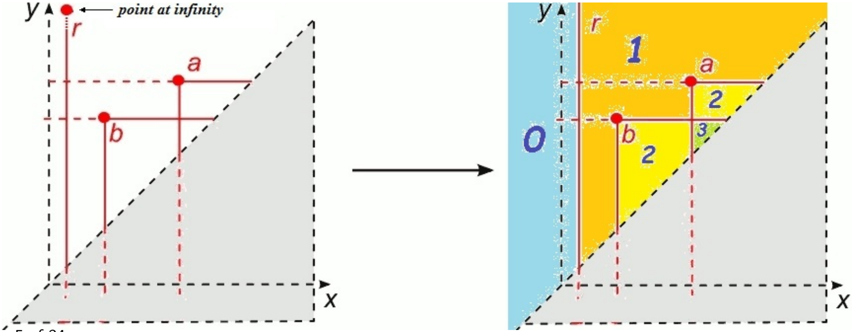
means that a class of a cycle exists

whose birth and death happen

at $\varphi = b$ and $\varphi = d$, respectively.

Persistence diagram $\leftrightarrow$ persistent Betti numbers

Under suitable technical assumptions (the use of Čech homology), persistence diagrams are equivalent to persistent Betti numbers functions. The persistent Betti numbers function of φ is the function $\beta_\varphi : \{x < y\} \to \mathbb{N} \cup \{\infty\}$ that counts how many points of $\mathrm{Dgm}(\varphi)$ are on the left and above the point (x, y).



Persistent Betti numbers functions

Equivalently, we can give this other definition:

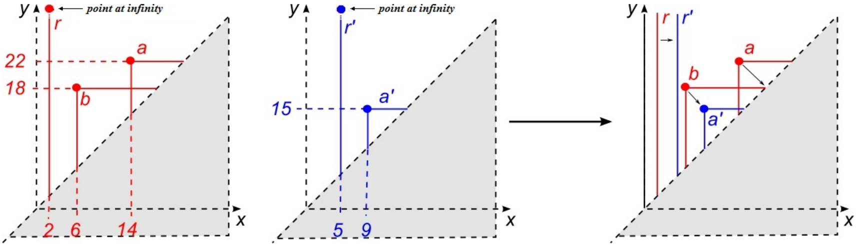
Definition

$\beta_\varphi(u, v)$ is the dimension of the persistent homology group computed at point (u, v), that is the rank of the homomorphism $i_k : H_k(X_u) \to H_k(X_v)$ induced by the inclusion $X_u := \{p \in X : \varphi(p) \le u\} \hookrightarrow X_v := \{p \in X : \varphi(p) \le v\}$, for $u < v$.

The matching distance d_{match}

Persistence diagrams can be compared by a matching distance d_{match}.

Roughly speaking, d_{match} quantifies the minimum cost of the matchings between two persistence diagrams, when the movements of points are measured by the maximum norm $\|(x,y)\|_\infty = \max(|x|,|y|)$. By definition, the movements along the diagonal $x = y$ have cost 0.



Persistent Betti numbers functions

What can we do in the case $f : X \to \mathbb{R}^2$?

If a function $f : X \to \mathbb{R}^2$ is given, we can still consider its persistent Betti numbers function β_f.

Definition

$\beta_f((u_1,u_2),(v_1,v_2))$ is the dimension of the persistent homology group computed at point $((u_1,u_2),(v_1,v_2))$, that is the rank of the homomorphism $i_k : H_k(X_{(u_1,u_2)}) \to H_k(X_{(v_1,v_2)})$ induced by the inclusion $X_{(u_1,u_2)} := \{p \in X : f_1(p) \leq u_1, f_2(p) \leq u_2\} \hookrightarrow X_{(v_1,v_2)} := \{p \in X : f_1(p) \leq v_1, f_2(p) \leq v_2\}$, for $u_1 < v_1, u_2 < v_2$.

Persistence diagram associated with the pair (P, w)

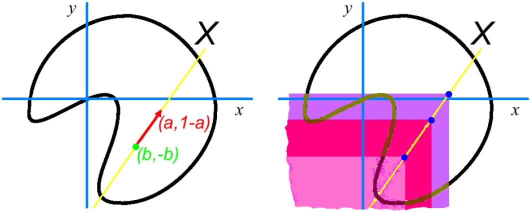
The approach based on persistent Betti numbers functions is equivalent to another approach based on an infinite family of persistence diagrams.

This has been proved in the paper

[A. Cerri, B. Di Fabio, M. Ferri, P. Frosini, C. Landi, Betti numbers in multidimensional persistent homology are stable functions, Mathematical Methods in the Applied Sciences, vol. 36 (2013), 1543-1557].

We recall this idea in the next slides.

Persistence diagram associated with the pair (P, w)



If we have a bifiltration given by a function $f = (f_1, f_2) : X \to \mathbb{R}^2$, we can consider a unit vector (w.r.t. $\|\cdot\|_1$) $w = (a, 1-a)$ with a positive slope, and a point $P = (b, -b)$. Every choice of P and w defines a filtration $\{X_t\}$ of X, where X_t is the set of points of X that are both under and on the left of the point $P + tw$. As a consequence, each choice of P and w defines a persistence diagram.

The normalized function $f^*_{(a,b)}$

If we set $(x,y) = P + tw = (at+b, (1-a)t-b)$ and define the function $f_{(a,b)}(p) := \max\left\{\frac{f_1(p)-b}{a}, \frac{f_2(p)+b}{1-a}\right\}$, we can write $X_t = \{p \in X : f_1(p) \le x, f_2(p) \le y\}$ as the set $\{p \in X : f_{(a,b)}(p) \le t\}$.
As a consequence, the filtration $\{X_t\}$ of X leads us to consider the persistence diagram $\mathrm{Dgm}(f_{(a,b)})$ of the function $f_{(a,b)}$.
In order to get a stability theorem we have to normalize $f_{(a,b)}$ by setting

$$f^*_{(a,b)}(p) := \min\{a, 1-a\} \cdot f_{(a,b)}(p).$$

The persistence diagram $\mathrm{Dgm}(f^*_{(a,b)})$ can be obtained by multiplying the persistence diagram $\mathrm{Dgm}(f_{(a,b)})$ by the value $\min\{a, 1-a\}$.

Stability of D_{match}

We can define a 2D matching distance $D_{\mathrm{match}}(\beta_f, \beta_g)$ between the persistent Betti number functions β_f and β_g by setting

$D_{\mathrm{match}}(\beta_f, \beta_g) := \sup_{(a,b)} d_{\mathrm{match}}\left(\mathrm{Dgm}(f^*_{(a,b)}), \mathrm{Dgm}(g^*_{(a,b)})\right).$

Theorem (Stability Theorem)

$D_{\mathrm{match}}(\beta_f, \beta_g) \leq \|f - g\|_\infty.$

Remark: The previous theorem strongly depends on the normalization of persistence diagrams.

The distance D_{match} has been introduced in the paper [S. Biasotti, A. Cerri, P. Frosini, D. Giorgi, C. Landi, Multidimensional size functions for shape comparison, Journal of Mathematical Imaging and Vision, vol. 32 (2008), n. 2, 161-179.]

Computation of the 2D matching distance

An algorithm to compute the 2D matching distance exists:

- S. Biasotti, A. Cerri, P. Frosini, D. Giorgi, A new algorithm for computing the 2-dimensional matching distance between size functions, Pattern Recognition Letters, vol. 32 (2011), n. 14, 1735-1746
- A. Cerri, P. Frosini, A new approximation algorithm for the matching distance in multidimensional persistence, AMS Acta, 2971 (2011)

Computation of the 2D matching distance

Remarks:

- In principle, 2D persistent homologies can be also compared by using the interleaving distance ([M. Lesnick, The theory of the interleaving distance on multidimensional persistence modules, Foundations of Computational Mathematics, vol. 15 (2015), n. 3, 613-650]). Unfortunately, as noted in that paper, the question of if and how the interleaving distance on multidimensional persistence modules can be computed remains open. This fact justifies the interest in the 2D matching distance D_{match}, which is easily computable.
- As for the visualization of 2D persistence modules we point out the interesting paper [M. Lesnick, M. Wright, Interactive Visualization of 2-D Persistence Modules, arXiv:1512.00180].

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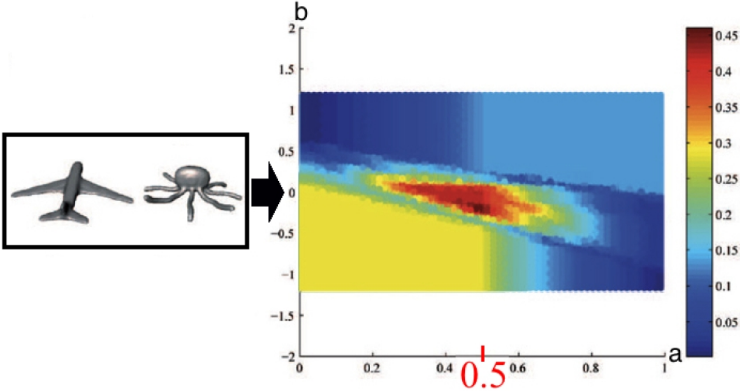
Some experiments in 3D shape comparison

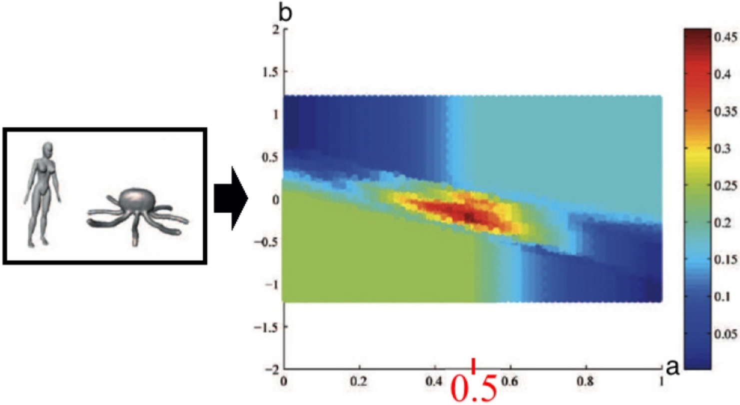
Let us have a look at some pictures illustrating some results that we have obtained in 3D shape comparison by means of the 2D matching distance. The objects that we compare are displayed on the left of each figure. The color at the point (a,b) represents the value $d_{\mathrm{match}}\left(\mathrm{Dgm}(f^*_{(a,b)}),\mathrm{Dgm}(g^*_{(a,b)})\right)$. The largest values are in **red** and **brown**, the lowest ones are in **blue**. The values at points (a,b) with $|b|$ large are not displayed, since they just represent the 1-dimensional persistence of the two components of $f=(f_1,f_2)$ and are not relevant for our exposition. We recall that we are interested in $D_{\mathrm{match}}(\beta_f,\beta_g)$, i.e. the supremum of $d_{\mathrm{match}}\left(\mathrm{Dgm}(f^*_{(a,b)}),\mathrm{Dgm}(g^*_{(a,b)})\right)$, for $0<a<1$ and $b\in\mathbb{R}$.

Some experiments in 3D shape comparison



Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with $a \approx 1/2$.

Some experiments in 3D shape comparison



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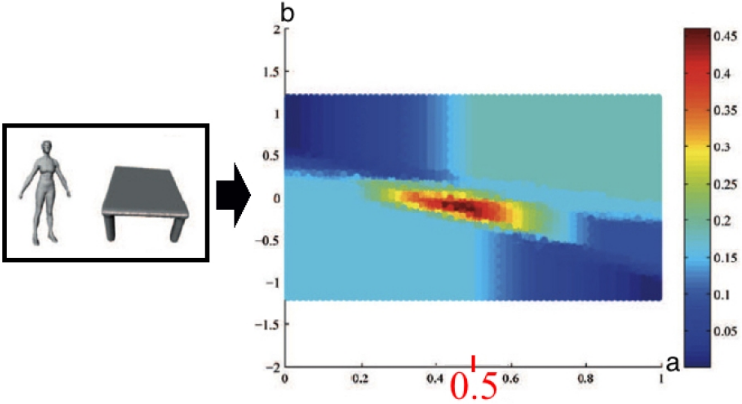
Some experiments in 3D shape comparison



Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with $a \approx 1/2$.

An interesting question

In our experiments, it seems that all the relevant information is given at points (a, b) with $a = 1/2$, i.e. in correspondence of lines with slope 1. At the beginning we thought that this phenomenon was just a coincidence. So we looked for other examples, showing global maxima at points (a, b) with $a \neq 1/2$, but our search was unsuccessful.

A natural question arises: Is there any interesting principle hidden in the results of our experiments?

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Some difficulties in our problem

Unfortunately, we are not able to directly answer this question, because of the lack of geometrical properties in the definition of D_{match}. Furthermore, we observe that while the metric D_{match} is rather simple to define and compute by considering a suitable family of filtering functions associated with lines having a positive slope, it has two main drawbacks.

- First, it forgets the natural link between the homological properties of filtrations associated with lines that are close to each other, so that part of the interesting homological information is lost.
- Second, its intrinsically discontinuous definition makes it difficult to study its properties.

A naïve (and wrong) solution to our problem

Our first (and naïve) idea was the one of defining a new distance, focusing on COHERENT matchings, i.e. matchings $\sigma_{(a,b)}$ that depend continuously on a and b. In order to build coherent matchings we tried to follow this approach:

- We should fix a pair $(\bar{a},\bar{b})$ and a matching $\sigma_{(\bar{a},\bar{b})}$ between the persistence diagrams $\mathrm{Dgm}(f^*_{(\bar{a},\bar{b})}), \mathrm{Dgm}(g^*_{(\bar{a},\bar{b})})$;
- Then we should construct a coherent family of matchings $\sigma_{(a,b)}$ between the persistence diagrams $\mathrm{Dgm}(f^*_{(a,b)}), \mathrm{Dgm}(g^*_{(a,b)})$, by "transporting $\sigma_{(\bar{a},\bar{b})}$ to any other point (a,b) in the parameter space by continuity";
- This transportation would use the stability of the normalized persistence diagrams $\mathrm{Dgm}(f^*_{(a,b)}), \mathrm{Dgm}(g^*_{(a,b)})$, i.e. the fact that they depend continuously on a and b.

A naïve (and wrong) solution to our problem

The previously proposed approach has a problem. If along the transportation we meet a point (a', b') at which one of the two normalized persistence diagrams contains a multiple point, then our transportation is not well-defined. Indeed, during "collisions" the identity of points is not preserved and we are not able to follow them. The consequent natural idea is the one of following the movements of points of $\mathrm{Dgm}(f^*_{(a,b)})$ and $\mathrm{Dgm}(g^*_{(a,b)})$ avoiding the pairs (a', b') for which points with multiplicity greater than one exist. We call these pairs singular. The other pairs are called regular.

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A key difficulty in our naïve solution

Unfortunately, the previous approach still has a problem.
Indeed, the definition of transport depends on the choice of the path γ that we follow in the parameter space. Precisely, this definition depends on the homotopy class of γ relative to the startpoint $(\bar{a}, \bar{b})$ and the endpoint (a, b).

We call this fact the monodromy phenomenon in 2-dimensional persistent homology.

For more details about the monodromy phenomenon in 2-dimensional persistent homology we refer to the paper
[A. Cerri, M. Ethier, P. Frosini, A study of monodromy in the computation of multidimensional persistence, Proceedings of the 17th IAPR International Conference on Discrete Geometry for Computer Imagery, LNCS 7749, 2013, 192-202].

An example of monodromy in 2D persistent homology

Let us see what happens if we consider the function $f = (f_1, f_2) : \mathbb{R}^2 \to \mathbb{R}^2$ obtained by setting

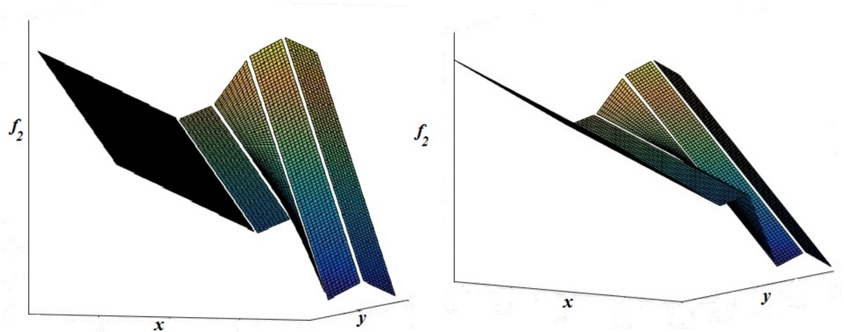
$$f_1(x,y) = x$$

$$f_2(x,y) := \begin{cases} -x, & \text{for } y = 0 \\ -x+1, & \text{for } y = 1 \\ -2x, & \text{for } y = 2 \\ -2x+\frac{5}{4}, & \text{for } y = 3 \end{cases}$$

$f_2(x,y)$ then being extended linearly for every x on the segment joining $(x,0)$ with $(x,1)$, $(x,1)$ with $(x,2)$, and $(x,2)$ to $(x,3)$. On the half-lines $\{(x,y) \in \mathbb{R}^2 : y < 0\}$ and $\{(x,y) \in \mathbb{R}^2 : y > 3\}$ f_2 is then being taken with constant slope 1 in the variable y.

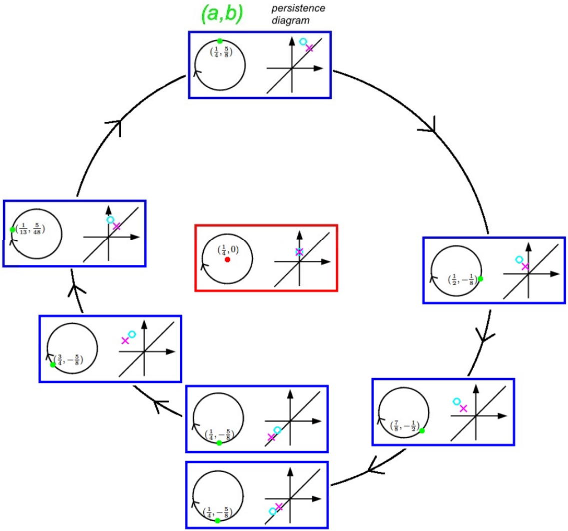
An example of monodromy in 2D persistent homology

The graph of the function f_2:



MonodromyVisualizer.jar

An example of monodromy in 2D persistent homology



An example of monodromy in 2D persistent homology

We have seen that if we turn around the point $(1/4, 0)$ in the parameter space $]0,1[\times\mathbb{R}$, two points in the persistence diagram $\mathrm{Dgm}(f^*_{(a,b)})$ exchange their position. In other words, a loop around the singular point $(1/4, 0)$ induces a permutation on the persistence diagram.

Therefore, a monodromy group is associated with the function f. In order to properly define this group, we have to give a precise definition of the path followed by a point $p \in \mathrm{Dgm}(f^*_{(a,b)})$ when (a, b) moves (and also when p meets Δ!) We will make this point precise in the next lecture.

Monodromy group of a function f

However, roughly speaking,

Definition

The persistent monodromy group of $f : M \to \mathbb{R}^2$ is the group of the permutations of $\mathrm{Dgm}(f^*_{(a,b)})$ induced by loops in the parameter space $]0,1[\times\mathbb{R}$.

Theorem

For every group of permutations G, a function $f : \mathbb{R}^2 \to \mathbb{R}^2$ exists such that its persistent monodromy group is G.

(Joint work with Nicolas Vercheval)

$a = 1/2?$

The existence of monodromy implies that different paths going from $(\bar{a}, \bar{b})$ to (a, b) can “transport matchings in different ways”.

Does monodromy prevent us from proceeding in our research and from defining a coherent 2-dimensional matching distance?

Fortunately, the answer is no, as we will show in the next lecture.

In the next lecture we will also come back to our question

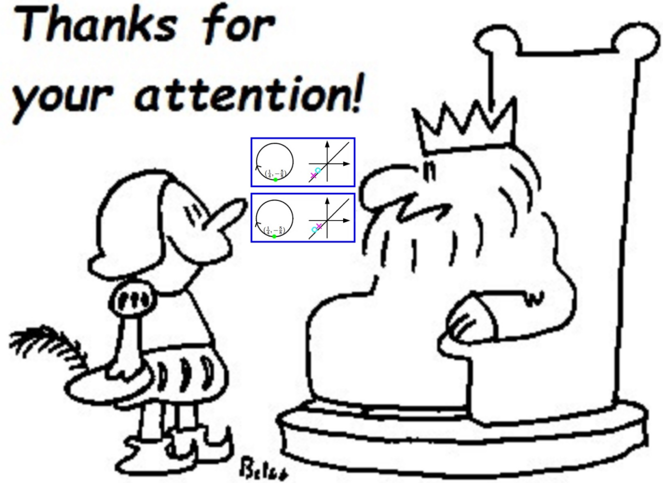
$$\boxed{a = 1/2?}$$

In order to face this problem we will have to introduce some mathematical machinery.

Conclusions

- In this lecture we have illustrated the phenomenon of monodromy in 2D persistent homology, which has been discovered in the attempt to prove the conjecture “$a = 1/2$”.
- Beyond the intrinsic interest of this phenomenon, it is also an obstruction to define a coherent matching distance between 2D persistent Betti numbers functions.
- In the next lecture we will see how we can manage this problem.

Thanks for your attention!



"A *round* trip, you say, Columbus?"